SEQUENCE LISTING

<110> De Buyl, Eric
Lahaye, Andree
Ledoux, Pierre
Detroz, Rene

<120> Xylanase, Microorganisms Producing it, DNA Molecules, Methods for Preparing this Xylanase and Uses of the Latter

<130> GC450-D1-US

<140> US 09/909,207
<141> 2001-07-19

<150> US 08/470,953
<151> 1995-06-06

<150> BE 09500448
<151> 1995-05-17

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<151> 1994-07-26

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<213> Bacillus sp.

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aacaatgtta acaacatatt attccgtaaa ggtaaaaaat tcaatgaaac acaaacacac 180
caacaagttg gtaacatgtc cataaactac ggagccaact tccaaccaaa tggtaatgcg 240
tatttatgcg tctatggttg gactgttgac cctcttgtcg aatattatat tgtcgacagt 300
tggggcaact ggcgtccacc aggagcaacg cctaagggga ccatcactgt tgatggagga 360
acatatgata tctacgagac tcttagagtc aatcaaccct ccattaaggg gattgccaca 420
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aaccacttta gagcgtggga aaacttaggg atgaatatgg ggaaaatgta tgaagtcgcg 540
cttactgtag aaggctatca aagtagcgga agtgctaatg tatatagcaa tacactaaga 600
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aat 663

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<213> Bacillus sp.

<220>
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<222> (1)...(663)

<221> mat_peptide
<222> (1)...(663)

<400> 2

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Gln Ile Val Thr Asp Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr
 1               5                  10                  15

gaa ttt tgg aaa gat agc ggt ggc tct ggg aca atg att ctc aat cat       96
Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His
            20                  25                  30

ggc ggt acg ttc agt gcc caa tgg aac aat gtt aac aac ata tta ttc      144
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe
        35                  40                  45

cgt aaa ggt aaa aaa ttc aat gaa aca caa aca cac caa caa gtt ggt      192
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly
    50                  55                  60

aac atg tcc ata aac tac gga gcc aac ttc caa cca aat ggt aat gcg      240
Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala
65                  70                  75                  80

tat tta tgc gtc tat ggt tgg act gtt gac cct ctt gtc gaa tat tat      288
Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr
                85                  90                  95

att gtc gac agt tgg ggc aac tgg cgt cca cca gga gca acg cct aag      336
Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys
            100                 105                 110

ggg acc atc act gtt gat gga gga aca tat gat atc tac gag act ctt      384
Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu
        115                 120                 125

aga gtc aat caa ccc tcc att aag ggg att gcc aca ttt aaa caa tat      432
Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr
    130                 135                 140

tgg agt gtt cga aga tcg aaa cgc acg agt ggc acg att tct gtc agc      480
Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser
145                 150                 155                 160

aac cac ttt aga gcg tgg gaa aac tta ggg atg aat atg ggg aaa atg      528
Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met
                165                 170                 175

tat gaa gtc gcg ctt act gta gaa ggc tat caa agt agc gga agt gct      576
Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala
            180                 185                 190

aat gta tat agc aat aca cta aga att aac ggt aac cct ctc tca act      624
Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr
        195                 200                 205
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att agt aat gac gag agc ata act ttg gat aaa aac aat                  663
Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn
    210                 215                 220
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<210> 3
<211> 221
<212> PRT
<213> Bacillus sp.

<400> 3

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            20                  25                  30
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe
        35                  40                  45
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly
    50                  55                  60
Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala
65                  70                  75                  80
Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr
                85                  90                  95
Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys
            100                 105                 110
Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu
        115                 120                 125
Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr
    130                 135                 140
Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser
145                 150                 155                 160
Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met
                165                 170                 175
Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala
            180                 185                 190
Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr
        195                 200                 205
Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn
    210                 215                 220
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<212> DNA
<213> Bacillus sp.

<400> 4

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tatgattatg aattttggaa agatagcggt ggctctggga caatgattct caatcatggc     180
ggtacgttca gtgcccaatg gaacaatgtt aacaacatat tattccgtaa aggtaaaaaa     240
ttcaatgaaa cacaaacaca ccaacaagtt ggtaacatgt ccataaacta cggagccaac     300
ttccaaccaa atggtaatgc gtatttatgc gtctatggtt ggactgttga ccctcttgtc     360
gaatattata ttgtcgacag ttggggcaac tggcgtccac caggagcaac gcctaagggg     420
accatcactg ttgatggagg aacatatgat atctacgaga ctcttagagt caatcaaccc     480
tccattaagg ggattgccac atttaaacaa tattggagtg ttcgaagatc gaaacgcacg     540
agtggcacga tttctgtcag caaccacttt agagcgtggg aaaacttagg gatgaatatg     600
gggaaaatgt atgaagtcgc gcttactgta gaaggctatc aaagtagcgg aagtgctaat     660
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gtatatagca atacactaag aattaacggt aacctctct caactattag taatgacgag      720
agcataactt tggataaaaa caat                                            744

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<213> Bacillus sp.

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Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala Phe Leu Val Cys Phe
 1               5                  10                  15

gca cta acc tta cct gca gaa ata att cag gca caa atc gtc acc gac       96
Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala Gln Ile Val Thr Asp
             20                  25                  30

aat tcc att ggc aac cac gat ggc tat gat tat gaa ttt tgg aaa gat      144
Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp
         35                  40                  45

agc ggt ggc tct ggg aca atg att ctc aat cat ggc ggt acg ttc agt      192
Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser
     50                  55                  60

gcc caa tgg aac aat gtt aac aac ata tta ttc cgt aaa ggt aaa aaa      240
Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys
 65                  70                  75                  80

ttc aat gaa aca caa aca cac caa caa gtt ggt aac atg tcc ata aac      288
Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn
                 85                  90                  95

tac gga gcc aac ttc caa cca aat ggt aat gcg tat tta tgc gtc tat      336
Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr
            100                 105                 110

ggt tgg act gtt gac cct ctt gtc gaa tat tat att gtc gac agt tgg      384
Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp
        115                 120                 125

ggc aac tgg cgt cca cca gga gca acg cct aag ggg acc atc act gtt      432
Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val
    130                 135                 140

gat gga gga aca tat gat atc tac gag act ctt aga gtc aat caa ccc      480
Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro
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145                 150                 155                 160

tcc att aag ggg att gcc aca ttt aaa caa tat tgg agt gtt cga aga      528
Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg
                165                 170                 175

tcg aaa cgc acg agt ggc acg att tct gtc agc aac cac ttt aga gcg      576
Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala
            180                 185                 190

tgg gaa aac tta ggg atg aat atg ggg aaa atg tat gaa gtc gcg ctt      624
Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu
        195                 200                 205

act gta gaa ggc tat caa agt agc gga agt gct aat gta tat agc aat      672
Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn
    210                 215                 220

aca cta aga att aac ggt aac cct ctc tca act att agt aat gac gag      720
Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu
225                 230                 235                 240

agc ata act ttg gat aaa aac aat                                     744
Ser Ile Thr Leu Asp Lys Asn Asn
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<210> 6
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<212> PRT
<213> Bacillus sp.

<400> 6

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 1               5                  10                  15
Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala Gln Ile Val Thr Asp
            20                  25                  30
Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp
        35                  40                  45
Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser
    50                  55                  60
Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys
65                  70                  75                  80
Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn
                85                  90                  95
Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr
            100                 105                 110
Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp
        115                 120                 125
Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val
    130                 135                 140
Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro
145                 150                 155                 160
Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg
                165                 170                 175
Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala
            180                 185                 190
```

```
Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu
        195                 200                 205
Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn
    210                 215                 220
Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu
225                 230                 235                 240
Ser Ile Thr Leu Asp Lys Asn Asn
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<212> DNA
<213> Bacillus sp.

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cctgcagaaa taattcaggc a 81

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<211> 81
<212> DNA
<213> Bacillus sp.

<220>
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<222> (1)...(81)

<221> sig_peptide
<222> (1)...(81)

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 1   5   10   15

gca cta acc tta cct gca gaa ata att cag gca 81
Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala
             20   25

<210> 9
<211> 27
<212> PRT
<213> Bacillus sp.

<400> 9
Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala Phe Leu Val Cys Phe
 1   5   10   15
Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala
            20   25

<210> 10
<211> 1513
<212> DNA
<213> Bacillus sp.

<400> 10

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ataggaactt tcccatttgc aagacgataa aaaatctttt tcccctattt tatcttatcg     180
ccttgatcgg tttaatttgt aaactttatt ttagtttacg tgatgttccc tcattcatac     240
cattaatcac agttaacgct agagtcatct tttttcggtt ctcaaaaata cctgaagaac     300
atttatgtca tattttctca cgccgctcca taatggaata tatatactct tttatacata     360
ttaagtaaat tagtatatac ttgcgttatc aaaatgtgag ataatctaat tgatcaaaca     420
agcagctatc caaaaaacac tgatgttgac ctcttaaaga agtgtcacta tctatgaaaa     480
gataattatc cagtttcaaa atttgaaata gtgtgtatgg aatagtttga atgtcaactg     540
ctgtgaaagg agggtaggta gtaccgtaga cttcattacc aaaaattagt tgtaaaaaaa     600
ttaaaaggag gaatgcctaa tgagacaaaa gaaattgacg ttgattttag ccttttttagt     660
ttgttttgca ctaaccttac ctgcagaaat aattcaggca caaatcgtca ccgacaattc     720
cattggcaac cacgatggct atgattatga attttggaaa gatagcggtg gctctgggac     780
aatgattctc aatcatggcg gtacgttcag tgcccaatgg aacaatgtta acaacatatt     840
attccgtaaa ggtaaaaaat tcaatgaaac acaaacacac caacaagttg gtaacatgtc     900
cataaactac ggagccaact tccaaccaaa tggtaatgcg tatttatgcg tctatggttg     960
gactgttgac cctcttgtcg aatattatat tgtcgacagt tggggcaact ggcgtccacc    1020
aggagcaacg cctaagggga ccatcactgt tgatggagga acatatgata tctacgagac    1080
tcttagagtc aatcaaccct ccattaaggg gattgccaca tttaaacaat attggagtgt    1140
tcgaagatcg aaacgcacga gtggcacgat ttctgtcagc aaccacttta gagcgtggga    1200
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aagtagcgga agtgctaatg tatatagcaa tacactaaga attaacggta accctctctc    1320
aactattagt aatgacgaga gcataacttt ggataaaaac aattaaaaat ccttatctct    1380
ttcggttcag ttctcattat tttcaaataa cctcccggtt ggatcttttc caacgggagg    1440
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<210> 11
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<212> DNA
<213> Bacillus sp.

<220>
<221> CDS
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<221> mat_peptide
<222> (701)...(1363)

<221> sig_peptide
<222> (620)...(700)

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ataggaactt tcccatttgc aagacgataa aaaatctttt tcccctattt tatcttatcg     180
ccttgatcgg tttaatttgt aaactttatt ttagtttacg tgatgttccc tcattcatac     240
cattaatcac agttaacgct agagtcatct tttttcggtt ctcaaaaata cctgaagaac     300
atttatgtca tattttctca cgccgctcca taatggaata tatatactct tttatacata     360
ttaagtaaat tagtatatac ttgcgttatc aaaatgtgag ataatctaat tgatcaaaca     420
agcagctatc caaaaaacac tgatgttgac ctcttaaaga agtgtcacta tctatgaaaa     480
gataattatc cagtttcaaa atttgaaata gtgtgtatgg aatagtttga atgtcaactg     540
ctgtgaaagg agggtaggta gtaccgtaga cttcattacc aaaaattagt tgtaaaaaaa     600
ttaaaaggag gaatgccta atg aga caa aag aaa ttg acg ttg att tta gcc      652
                    Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala
                     1               5                  10
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ttt tta gtt tgt ttt gca cta acc tta cct gca gaa ata att cag gca      700
Phe Leu Val Cys Phe Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala
             15                  20                  25

caa atc gtc acc gac aat tcc att ggc aac cac gat ggc tat gat tat      748
Gln Ile Val Thr Asp Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr
         30                  35                  40

gaa ttt tgg aaa gat agc ggt ggc tct ggg aca atg att ctc aat cat      796
Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His
     45                  50                  55

ggc ggt acg ttc agt gcc caa tgg aac aat gtt aac aac ata tta ttc      844
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe
 60                  65                  70                  75

cgt aaa ggt aaa aaa ttc aat gaa aca caa aca cac caa caa gtt ggt      892
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly
                 80                  85                  90

aac atg tcc ata aac tac gga gcc aac ttc caa cca aat ggt aat gcg      940
Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala
             95                 100                 105

tat tta tgc gtc tat ggt tgg act gtt gac cct ctt gtc gaa tat tat      988
Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr
        110                 115                 120

att gtc gac agt tgg ggc aac tgg cgt cca cca gga gca acg cct aag     1036
Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys
    125                 130                 135

ggg acc atc act gtt gat gga gga aca tat gat atc tac gag act ctt     1084
Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu
140                 145                 150                 155

aga gtc aat caa ccc tcc att aag ggg att gcc aca ttt aaa caa tat     1132
Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr
                160                 165                 170

tgg agt gtt cga aga tcg aaa cgc acg agt ggc acg att tct gtc agc     1180
Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser
            175                 180                 185

aac cac ttt aga gcg tgg gaa aac tta ggg atg aat atg ggg aaa atg     1228
Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met
        190                 195                 200

tat gaa gtc gcg ctt act gta gaa ggc tat caa agt agc gga agt gct     1276
Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala
    205                 210                 215

aat gta tat agc aat aca cta aga att aac ggt aac cct ctc tca act     1324
Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr
220                 225                 230                 235

att agt aat gac gag agc ata act ttg gat aaa aac aat taaaaatcct      1373
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Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn
240 245

tatctctttc ggttcagttc tcattatttt caaataacct cccggttgga tcttttccaa 1433
cgggaggttt tattggaaag gttaagtata gtatactccg attccatcca gaggaatgct 1493
tgaaacacct ccgtcactag 1513

<210> 12
<211> 619
<212> DNA
<213> Bacillus sp.

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aaaccaatac ttctttattt aacgctaacc acttgcaatc ttatcacaag aacattcttt 120
ataggaactt tcccatttgc aagacgataa aaaatctttt tcccctattt tatcttatcg 180
ccttgatcgg tttaatttgt aaactttatt ttagtttacg tgatgttccc tcattcatac 240
cattaatcac agttaacgct agagtcatct tttttcggtt ctcaaaaata cctgaagaac 300
atttatgtca tattttctca cgccgctcca taatggaata tatatactct tttatacata 360
ttaagtaaat tagtatatac ttgcgttatc aaaatgtgag ataatctaat tgatcaaaca 420
agcagctatc caaaaaacac tgatgttgac ctcttaaaga agtgtcacta tctatgaaaa 480
gataattatc cagtttcaaa atttgaaata gtgtgtatgg aatagtttga atgtcaactg 540
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ttaaaaggag gaatgccta 619

<210> 13
<211> 150
<212> DNA
<213> Bacillus sp.

<400> 13
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gaggaatgct tgaaacacct ccgtcactag 150

<210> 14
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 14
ccccctacg tagcggccgc cccggccggt aacctaggaa gtcagcgccc tgcacc 56

<210> 15
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 15
ccccctacg taggccgggg cggccgcggt tacctagggc ctcgtgatac gcctat 56

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 16
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<210> 17
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 17
taccttgtct acaaacccc 19

<210> 18
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 18
cggtcgccgc atacacta 18

<210> 19
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<400> 19
ccccccccg gtaacctgca ttaatgaatc ggccaa 36

<210> 20
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<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 20
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<210> 21
<211> 50

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 21
ccccccctcta gattaattaa ccaagcttgg gatccgtcga cctgcagatc 50

<210> 22
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ggaaa 185

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<212> DNA
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<400> 27
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acggctgtgc cggctcatgc g 81

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<212> DNA
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<400> 28
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1 5 10 15

gtg ctg aca ctg acg gct gtg ccg gct cat gcg 81
Val Leu Thr Leu Thr Ala Val Pro Ala His Ala
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1 5 10 15
Val Leu Thr Leu Thr Ala Val Pro Ala His Ala
20 25